In the Claims

Claims 1-83 (Canceled).

Claim 84 (New): An *in vitro* hybridization method comprising:

(i) contacting a nucleic acid sample derived from a human subject with at least a pair of oligonucleotides, one being designated a 3' oligonucleotide and the other a 5' oligonucleotide, under hybridizing conditions wherein;

(a) the 5' oligonucleotide comprises the sequence of SEQ ID NO: 1, and at least one 3' oligonucleotide selected from the group of 3' oligonucleotides comprising the sequence of SEQ ID NO: 5, NO: 2, NO: 6 or NO: 7; or

(b) the 5' oligonucleotide comprises the sequence of SEQ ID NO: 4 and at least one 3' oligonucleotide comprising the sequence of SEQ ID NO: 5, NO: 2, NO: 6 or NO: 7; or

(c) the 5' oligonucleotide comprises the sequence of SEQ ID NO: 9 and at least one 3' oligonucleotide selected from the group of 3' oligonucleotides comprising the sequence SEQ ID NO: 5, NO: 2, NO: 6 or NO: 7, or

(d) at least one 5' oligonucleotide comprising the sequence of SEQ ID NO:10, NO: 11, NO: 12 or NO:13 and a 3' oligonucleotide comprising the sequence SEQ ID NO: 14; and

(ii) detecting hybridization between the nucleic acid sample and said at least a pair of oligonucleotides.

Claim 85 (New): The method of claim 84, wherein the nucleic acid sample is derived from blood, bone marrow, lymphocytes, NK and T cells, NK cells, T cells or transgenic cells.

Claim 86 (New): The method of claim 84, wherein the nucleic sample is a genomic or cDNA library.

Claim 87 (New): The method of claim 84, wherein hybridization between the nucleic acid sample and the 3' and 5' oligonucleotide pair is detected by PCR amplification.

Claim 88 (New): The method of claim 87, wherein said PCR amplification is nested PCR.

Claim 89 (New): The method of claim 84, wherein the hybridization between the nucleic acid and the 3' and 5' oligonucleotide pairs is detected by resolution and visualization on a polyacrylamide gel and visualization of electrophoretic bands containing the said hybrids.

Claim 90 (New): An *in vitro* hybridization method comprising:

(i) contacting a nucleic acid sample derived from a human subject with at least a pair of oligonucleotides, one being designated a 3' oligonucleotide and the other a 5' oligonucleotide, wherein:

(a) the 3' oligonucleotide of said oligonucleotide pair hybridizes to a nucleic acid encoding the amino acid sequence Lys Ile Pro Phe Thr Ile (K I P F T I) or Lys Leu Pro Phe Thr Ile (K L P F T I) (SEQ ID NO: 26 or 27); or

(b) the 5' oligonucleotide comprises the sequence of SEQ ID NO: 1 and a 3' oligonucleotide comprises the sequence of SEQ ID NO: 3; or

(c) the 5' oligonucleotide comprises the sequence of SEQ ID NO: 8 and a 3' oligonucleotide comprises the sequence of SEQ ID NO: 3; or

(d) the 5' oligonucleotide comprises the sequence of SEQ ID NO: 9 and a 3' oligonucleotide comprises the sequence SEQ ID NO: 3; or

(e) the 5' oligonucleotide comprises the sequence of SEQ ID NO: 15 and a 3' oligonucleotide comprises the sequence SEQ ID NO: 13; and

(ii) detecting hybridization between said nucleic acid sample and said at least a pair of oligonucleotides.

Claim 91 (New): The method of claim 90, wherein the nucleic acid sample is derived from blood, bone marrow, lymphocytes, NK and T cells, NK cells, T cells or transgenic cells.

Claim 92 (New): The method of claim 90, wherein the nucleic sample is a genomic or cDNA library.

Claim 93 (New): The method of claim 90, wherein hybridization between the nucleic acid sample and the 3' and 5' oligonucleotide pair is detected by PCR amplification.

Claim 94 (New): The method of claim 90, wherein said PCR amplification is nested PCR.

Claim 95 (New): The method of claim 90, wherein the hybridization between the nucleic acid and the 3' and 5' oligonucleotide pairs is detected by resolution and visualization on a polyacrylamide gel and visualization of electrophoretic bands containing the said hybrids.

Claim 96 (New): An *in vitro* hybridization method comprising:

(i) contacting a nucleic acid sample derived from a human said subject with at least a pair of oligonucleotides, one being designated a 3' oligonucleotide and the other a 5' oligonucleotide, wherein said 3' and 5' oligonucleotide pairs are selected from the group consisting of:

(a) a 5' oligonucleotide comprising the sequence of SEQ ID NO: 16 and a 3' oligonucleotide comprising the sequence SEQ ID NO: 17;

(b) a 5' oligonucleotide comprising the sequence of SEQ ID NO: 18 and a 3' oligonucleotide comprising the sequence SEQ ID NO: 17;

(c) a 5' oligonucleotide comprising the sequence of SEQ ID NO: 19 and a 3' oligonucleotide comprising the sequence SEQ ID NO: 17; and

(d) a 5' oligonucleotide comprising the sequence of SEQ ID NO: 20 and a 3' oligonucleotide comprising the sequence SEQ ID NO: 21; and

(ii) detecting the hybridization of said nucleic acid sample with said at least a pair of oligonucleotides.

Claim 97 (New): The method of claim 96, wherein the nucleic acid sample is derived from blood, bone marrow, lymphocytes, NK and T cells, NK cells, T cells or transgenic cells.

Claim 98 (New): The method of claim 96, wherein the nucleic sample is a genomic or cDNA library.

Claim 99 (New): The method of claim 96, wherein hybridization between the nucleic acid sample and the 3' and 5' oligonucleotide pair is detected by PCR amplification.

Claim 100 (New): The method of claim 99, wherein said PCR amplification is nested PCR.

Claim 101 (New): The method of claim 96, wherein the hybridization between the nucleic acid and the 3' and 5' oligonucleotide pairs is detected by resolution and visualization on a polyacrylamide gel and visualization of electrophoretic bands containing the said hybrids.

Claim 102 (New): An *in vitro* hybridization method comprising:

(i) contacting a nucleic acid sample derived from a human subject with at least a pair of oligonucleotides, one being designated a 3' oligonucleotide and the other a 5' oligonucleotide, wherein said 3' and 5' oligonucleotide pairs are selected from the group consisting of:

(a) a 5' oligonucleotide comprising the sequence of SEQ ID NO: 16 and a 3' oligonucleotide comprising the sequence SEQ ID NO: 17;

(b) a 5' oligonucleotide comprising the sequence of SEQ ID NO: 18 and a 3' oligonucleotide comprising the sequence SEQ ID NO: 17;

(c) a 5' oligonucleotide comprising the sequence of SEQ ID NO: 19 and a 3' oligonucleotide comprising the sequence SEQ ID NO: 17; and

(d) a 5' oligonucleotide comprising the sequence of SEQ ID NO: 20 and a 3' oligonucleotide comprising the sequence SEQ ID NO: 21; and

(ii) detecting the hybridization of said nucleic acid sample with said at least a pair of oligonucleotides.

Claim 103 (New): The method of claim 102, wherein the nucleic acid sample is derived from blood, bone marrow, lymphocytes, NK and T cells, NK cells, T cells or transgenic cells.

Claim 104 (New): The method of claim 102, wherein the nucleic sample is a genomic or cDNA library.

Claim 105 (New): The method of claim 102, wherein hybridization between the nucleic acid sample and the 3' and 5' oligonucleotide pair is detected by PCR amplification.

Claim 106 (New): The method of claim 105, wherein said PCR amplification is nested PCR.

Claim 107 (New): The method of claim 102, wherein the hybridization between the nucleic acid and the 3' and 5' oligonucleotide pairs is detected by resolution and visualization on a polyacrylamide gel and visualization of electrophoretic bands containing the said hybrids.

Claim 108 (New): A kit comprising a container, reagents for carrying out said hybridization methods, and at least one 3' and 5' oligonucleotide selected from the group consisting of:

5' oligonucleotide sequences comprising: SEQ ID NO: 1, 4, 8, 9, 10, 11, 12, 13, 15, 16, 18, 19, or 20; and

3' oligonucleotide sequences comprising SEQ ID NO: 2, 3, 5, 6, 7, 13, 14, 17, 21, a nucleic acid sequence encoding the polypeptide of SEQ ID NO: 26, or a nucleic acid sequence encoding the polypeptide of SEQ ID NO: 27.

Claim 109 (New): The kit according to claim 108, wherein the 3' or 5' oligonucleotides are coupled to a marker.

Claim 110 (New): The kit according to claim 108, wherein the marker is a fluorescent marker.

Claim 111 (New): The kit according to claim 108, wherein said at least one 3' and 5' oligonucleotide is selected from the group consisting of:

5' oligonucleotide sequences consisting of: SEQ ID NO: 1, 4, 8, 9, 10, 11, 12, 13, 15, 16, 18, 19, or 20; and

3' oligonucleotide sequences consisting of SEQ ID NO: 2, 3, 5, 6, 7, 13, 14, 17, 21, a nucleic acid sequence encoding the polypeptide of SEQ ID NO: 26, or a nucleic acid sequence encoding the polypeptide of SEQ ID NO: 27.

Claim 112 (New): The kit according to claim 111, wherein the 3' or 5' oligonucleotides are coupled to a marker.

Claim 113 (New): The kit according to claim 112, wherein the marker is a fluorescent marker.

Claim 114 (New): The kit according to claim 112, wherein the marker is a radioactive marker.

Claim 115 (New): The kit according to claim 109, wherein the marker is a radioactive marker.

Claim 116 (New): An *in vitro* method for identifying the repertoire of Natural Killer Receptor (NKR) immunoreceptors comprising:

(i) preparing at least a pair of oligonucleotides, at least one being designated a 3' oligonucleotide and at least one other being designated a 5' oligonucleotide, comprising a consensus sequence obtained from the alignment of cDNA sequences encoding a target NKR immunoreceptor, said consensus sequence being unable to hybridize with the DNA or cDNA sequence of a NKR immunoreceptor counterpart;

(ii) contacting a nucleic acid sample derived from a human subject with said at least a pair of oligonucleotides under hybridizing conditions; and

(iii) detecting hybridization between the nucleic acid sample and said at least a pair of oligonucleotides.

Claim 117 (New): The method according to claim 116, wherein said contacting step comprises contacting said nucleic acid sample and said at least a pair of oligonucleotides in a buffer comprising 20 mM Tris-NCl; 50 mM KCl; 2.5 mM $MgCl_2$ at a pH of 8.4 and at a temperature of between 50°C and 65°C.

Claim 118 (New): The method according to claim 116, wherein said target NKR immunoreceptor is p58.1 and said NKR counterpart receptor is p50.1.

Claim 119 (New): The method according to claim 116, wherein said target NKR immunoreceptor is p58.2 and said NKR counterpart receptor is p50.2.

Claim 120 (New): The method according to claim 116, wherein said target NKR immunoreceptor is p70.INH and said NKR counterpart receptor is p70.ACT.

Claim 121 (New): The method according to claim 116, wherein said target NKR immunoreceptor is p140.INH and said NKR counterpart receptor is p140.ACT.

Claim 122 (New): The method according to claim 116, wherein said target NKR immunoreceptor is NKG2A or NKG2B and said NKR counterpart receptor is NKG2C, NKG2D, NKG2E, or NKG2F.

Claim 123 (New): The method according to claim 116, wherein said consensus sequence is obtained from the alignment of the cDNA of GenBank Accession Number(s): a) U24076, L41267, and U24078; b) X98585, X98892, L76670, and L76672; c) U24075, L76669, L76663, U24074, L41268, U73395, L76662, and L76664; d) U24079, L41347, X89893, U24077, L76671, and L76667; e) X94262, L41269, U31416, U33328, U71199, U73394, X94373, U30274, and U30273; f) L76661 and U73396; or g) L41270, X94374, X93595, X93596, L76666, L76665, and U30272.

Claim 124 (New): The method according to claim 116, wherein said NKR immunoreceptor repertoire contains one or more NKR immunoreceptor selected from:

a) p58.1 encodable by GenBank Accession Number U24076, L41267 or U24078;

b) p50.1 encodable by GenBank Accession Number X98585, X98892, L76670 or L76672;

c) p58.2 encodable by GenBank Accession Number U24075, L76669, L76663, U24074, L41268, U73395, L76662 or L76664;

d) p50.2 encodable by GenBank Accession Number U24079, L41347, X89893, U24077, L76671 or L76667;

e) p70.INH encodable by GenBank Accession Number X94262, L41269, U31416, U33328, U71199, U73394, X94373, U30274 or U30273;

f) p70.ACT encodable by GenBank Accession Number L76661 or U73396;

g) p140.INH encodable by GenBank Accession Number L41270, X94374, X93595, X93596, L76666, L76665 or U30272;

h) NKG2A encodable by GenBank Accession Number X54867;

i) NKG2B encodable by GenBank Accession Number X54868;

j) NKG2C encodable by GenBank Accession Number X54869; and

k) NKG2D encodable by GenBank Accession Number X54870.